

RESULT 2

FACE2_MOUSE

ID FACE2_MOUSE STANDARD; PRT; 329 AA.
AC P57791; Q9CSF8; Q9EP68;
DT 27-APR-2001, integrated into UniProtKB/Swiss-Prot.
DT 27-APR-2001, sequence version 1.
DT 07-FEB-2006, entry version 33.
DE CAAX prenyl protease 2 (EC 3.4.22.-) (Prenyl protein-specific
DE endoprotease 2) (Farnesylated proteins-converting enzyme 2) (FACE-2).
GN Name=Rce1; Synonyms=Face2, Rcela;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cadinanos J., Freije J.M.P.;
RT "Characterization and expression analysis of the gene encoding the
RT murine Caax protease Face-2.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 15-329.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminieccki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP KNOCK-OUT.
RX MEDLINE=99185053; PubMed=10085069; DOI=10.1074/jbc.274.13.8383;
RA Kim E., Ambroziak P., Otto J.C., Taylor B., Ashby M., Shannon K.,
RA Casey P.J., Young S.G.;
RT "Disruption of the mouse Rce1 gene results in defective Ras processing
RT and mislocalization of Ras within cells.";

RL J. Biol. Chem. 274:8383-8390(1999).
 CC !- FUNCTION: Proteolytically removes the C-terminal three residues of
 CC farnesylated and geranylated proteins. Seems to be able to process
 CC K-Ras, N-Ras, H-Ras, RAP1B and G-gamma-1 (By similarity).
 CC !- SUBCELLULAR LOCATION: Endoplasmic reticulum; endoplasmic reticulum
 CC membrane; multi-pass membrane protein (By similarity).
 CC !- SIMILARITY: Belongs to the peptidase U48 family.
 CC -----
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 CC -----
 DR EMBL; AJ251644; CAC17013.1; -; Genomic_DNA.
 DR EMBL; AJ251645; CAC17014.1; -; mRNA.
 DR EMBL; AK012946; BAB28566.1; -; mRNA.
 DR MEROPS; U48.002; -.
 DR Ensembl; ENSMUSG00000024889; Mus musculus.
 DR MGI; MGI:1336895; Rcel.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR003675; Abi.
 DR Pfam; PF02517; Abi; 1.
 KW Endoplasmic reticulum; Hydrolase; Membrane; Transmembrane.
 FT CHAIN 1 329 CAAX prenyl protease 2.
 FT /FTId=PRO_0000194831.
 FT TRANSMEM 36 56 Potential.
 FT TRANSMEM 75 95 Potential.
 FT TRANSMEM 112 132 Potential.
 FT TRANSMEM 193 213 Potential.
 FT TRANSMEM 226 246 Potential.
 FT TRANSMEM 254 274 Potential.
 FT TRANSMEM 282 302 Potential.
 FT CONFLICT 17 27 PERQPESAALS -> QSGTRVSRAE (in Ref. 2).
 FT CONFLICT 62 62 R -> K (in Ref. 2).
 SQ SEQUENCE 329 AA; 35867 MW; C2A49617EDC77EC8 CRC64;

Alignment Scores:

Pred. No.:	2.87e-55	Length:	329
Score:	629.00	Matches:	123
Percent Similarity:	99.2%	Conservative:	0
Best Local Similarity:	99.2%	Mismatches:	1
Query Match:	89.2%	Indels:	1
DB:	1	Gaps:	0

US-10-646-950-5 (1-373) x FACE2_MOUSE (1-329)

Qy	1	TTTGGAGTCGCCCCATTTTCACCACATTATTGAGCAGCTGCGCTCCGCCAGAGCAGTGTG	60
Db	204	PheGlyValAlaHisPheHisHisIleIleGluGlnLeuArgPheArgGlnSerSerVal	223
Qy	61	GGAAGTATCTTCGTGTCTGCAGCGTTCCAGTTCTCTACACCGCTGTCTTCGGTGCTTAT	120
Db	224	GlySerIlePheValSerAlaAlaPheGlnPheSerTyrThrAlaValPheGlyAlaTyr	243
Qy	121	ACAGCTTTCTCTTCATCCGCACAGGACACCTGATAGGGCCGGTTCTCTGCCACTCTTTC	180
Db	244	ThrAlaPheLeuPheIleArgThrGlyHisLeuIleGlyProValLeuCysHisSerPhe	263
Qy	181	TGCAACTACATGGGCTTCCTGCAGTGTGTGCAGCCCTGGAGCATCCACAGAAGTGGCCA	240
Db	264	CysAsnTyrMetGlyPheProAlaValCysAlaAlaLeuGluHisProGlnLysTrpPro	283
Qy	241	CTGCTGGCAGGCTATGC-CTCGGTGTGGGACTTTTCCTGCTTCTGCTTCAACCCCTGACA	299
Db	284	LeuLeuAlaGlyTyrAlaLeuGlyValGlyLeuPheLeuLeuLeuGlnProLeuThr	303
Qy	300	GACCCCAAGCTCTATGGCAGCCTTCTCTTTGTATGCTTTTGGAAAGAACAGGGGCCTCA	359
Db	304	AspProLysLeuTyrGlySerLeuProLeuCysMetLeuLeuGluArgThrGlyAlaSer	323
Qy	360	GAGACCCTACTG	371
Db	324	GluThrLeuLeu	327